



SEQUENCE LISTING

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Freidrich, Glenn A.
Sands, Arthur T.

<120> A NOVEL HUMAN cDNA CLONE AND PROTEINS
ENCODED THEREBY

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<212> DNA

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<220>

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Trp Glu Thr Arg Val Lys Lys His Lys Ala Trp Gln Lys Lys Glu Val	
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gaa agg ctt gag aag agc gcc ttg gag aag ata aag gag gag tgg aac	144
Glu Arg Leu Glu Lys Ser Ala Leu Glu Lys Ile Lys Glu Glu Trp Asn	
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ttt gtg gcc gaa tgc agg agg aag ggc atc ccc cag gct gta tac tgc	192
Phe Val Ala Glu Cys Arg Arg Lys Gly Ile Pro Gln Ala Val Tyr Cys	
50 55 60	
aag aat ggc ttc ata gac acc agc gtg cgg ctt ctg gac aag att gaa	240
Lys Asn Gly Phe Ile Asp Thr Ser Val Arg Leu Leu Asp Lys Ile Glu	
65 70 75 80	
agg aac act ctc aca agg cag agt tca ctt ccc aag gac aga ggc aaa	288
Arg Asn Thr Leu Thr Arg Gln Ser Ser Leu Pro Lys Asp Arg Gly Lys	
85 90 95	
cgg agc agt gcg ttt gtg ttt gaa ctt tct ggg gag cac tgg acg gag	336
Arg Ser Ser Ala Phe Val Phe Glu Leu Ser Gly Glu His Trp Thr Glu	
100 105 110	
ctc cca gat tca ttg aag gag cag aca cac ctg aga gaa tgg tac ata	384
Leu Pro Asp Ser Leu Lys Glu Gln Thr His Leu Arg Glu Trp Tyr Ile	
115 120 125	
agc aat acc ttg att caa atc att cct aca tat att cag tta ttt caa	432
Ser Asn Thr Leu Ile Gln Ile Ile Pro Thr Tyr Ile Gln Leu Phe Gln	
130 135 140	

gcg atg aga att ctg gat ctg cca aaa aac caa atc tca cat ctt cca Ala Met Arg Ile Leu Asp Leu Pro Lys Asn Gln Ile Ser His Leu Pro 145 150 155 160	480
gca gaa atc ggt tgt ttg aag aac ctg aaa gaa ctc aat gtg ggt ttc Ala Glu Ile Gly Cys Leu Lys Asn Leu Lys Glu Leu Asn Val Gly Phe 165 170 175	528
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gag aga ctg gat tgt tct gga aat cta gaa tta atg gag ctg ccc ttt Glu Arg Leu Asp Cys Ser Gly Asn Leu Glu Leu Met Glu Leu Pro Phe 195 200 205	624
gaa tta agt aat ttg aag caa gtt aca ttt gta gat atc tca gca aac Glu Leu Ser Asn Leu Lys Gln Val Thr Phe Val Asp Ile Ser Ala Asn 210 215 220	672
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 Phe Val Ala Glu Cys Arg Arg Lys Gly Ile Pro Gln Ala Val Tyr Cys
 50 55 60
 Lys Asn Gly Phe Ile Asp Thr Ser Val Arg Leu Leu Asp Lys Ile Glu
 65 70 75 80
 Arg Asn Thr Leu Thr Arg Gln Ser Ser Leu Pro Lys Asp Arg Gly Lys
 85 90 95
 Arg Ser Ser Ala Phe Val Phe Glu Leu Ser Gly Glu His Trp Thr Glu
 100 105 110
 Leu Pro Asp Ser Leu Lys Glu Gln Thr His Leu Arg Glu Trp Tyr Ile
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 Ser Asn Thr Leu Ile Gln Ile Ile Pro Thr Tyr Ile Gln Leu Phe Gln
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 165 170 175
 Asn Tyr Leu Lys Ser Ile Pro Pro Glu Leu Gly Asp Cys Glu Asn Leu
 180 185 190
 Glu Arg Leu Asp Cys Ser Gly Asn Leu Glu Leu Met Glu Leu Pro Phe
 195 200 205
 Glu Leu Ser Asn Leu Lys Gln Val Thr Phe Val Asp Ile Ser Ala Asn
 210 215 220
 Lys Phe Ser Ser Val Pro Ile Cys Val Leu Arg Met Ser Asn Leu Gln
 225 230 235 240
 Trp Leu Asp Ile Ser Ser Asn Asn Leu Thr Asp Leu Pro Gln Asp Ile
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 Asp Arg Leu Glu Glu Leu Gln Ser Phe Leu Leu Tyr Lys Asn Lys Leu
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 Thr Tyr Leu Pro Tyr Ser Met Leu Asn Leu Lys Lys Leu Thr Leu Leu
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 Ser Ser Thr Pro Leu Lys Phe Val Ser Leu Met Asp Asn Pro Ile Asp
 305 310 315 320
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 325 330 335
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gaa atc ggt tgt ttg aag aac ctg aaa gaa ctc aat gtg ggt ttc aac	96
Glu Ile Gly Cys Leu Lys Asn Leu Lys Glu Leu Asn Val Gly Phe Asn	
20 25 30	
tat ctg aag agc att cct cca gaa ttg gga gat tgt gaa aat cta gag	144
Tyr Leu Lys Ser Ile Pro Pro Glu Leu Gly Asp Cys Glu Asn Leu Glu	
35 40 45	
aga ctg gat tgt tct gga aat cta gaa tta atg gag ctg ccc ttt gaa	192
Arg Leu Asp Cys Ser Gly Asn Leu Glu Leu Met Glu Leu Pro Phe Glu	
50 55 60	
tta agt aat ttg aag caa gtt aca ttt gta gat atc tca gca aac aag	240
Leu Ser Asn Leu Lys Gln Val Thr Phe Val Asp Ile Ser Ala Asn Lys	
65 70 75 80	
ttt tcc agt gtc cca atc tgt gtc ctg cgg atg tcg aat ttg cag tgg	288
Phe Ser Ser Val Pro Ile Cys Val Leu Arg Met Ser Asn Leu Gln Trp	
85 90 95	
ttg gat atc agc agc aat aac ctg acc gac ctg ccg caa gat ata gac	336
Leu Asp Ile Ser Ser Asn Asn Leu Thr Asp Leu Pro Gln Asp Ile Asp	
100 105 110	
agg cta gag gag ctg cag agc ttt ctc ttg tat aaa aac aag ttg acc	384
Arg Leu Glu Glu Leu Gln Ser Phe Leu Leu Tyr Lys Asn Lys Leu Thr	
115 120 125	
tac ctt ccc tat tcc atg ctg aac ctg aag aag ctc act ctg tta gtc	432
Tyr Leu Pro Tyr Ser Met Leu Asn Leu Lys Lys Leu Thr Leu Leu Val	
130 135 140	
gtc agt ggg gac cat ttg gtg gag ctc cca act gcc ctt tgt gac tca	480
Val Ser Gly Asp His Leu Val Glu Leu Pro Thr Ala Leu Cys Asp Ser	
145 150 155 160	
tcc aca cct tta aaa ttt gta agc ctt atg gac aat cct att gat aat	528
Ser Thr Pro Leu Lys Phe Val Ser Leu Met Asp Asn Pro Ile Asp Asn	
165 170 175	
gcc caa tgt gaa gat ggc aat gaa ata atg gaa agt gaa cgg gat cgc	576
Ala Gln Cys Glu Asp Gly Asn Glu Ile Met Glu Ser Glu Arg Asp Arg	
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caa cat ttt gat aaa gaa gtt atg aaa gcc tat att gaa gac ctt aaa	624
Gln His Phe Asp Lys Glu Val Met Lys Ala Tyr Ile Glu Asp Leu Lys	
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gaa aga gaa tct gtt ccc agc tat acc acc aaa gtg tct ttt agc ctt	672
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 Arg Leu Asp Cys Ser Gly Asn Leu Glu Leu Met Glu Leu Pro Phe Glu
 50 55 60
 Leu Ser Asn Leu Lys Gln Val Thr Phe Val Asp Ile Ser Ala Asn Lys
 65 70 75 80
 Phe Ser Ser Val Pro Ile Cys Val Leu Arg Met Ser Asn Leu Gln Trp
 85 90 95
 Leu Asp Ile Ser Ser Asn Asn Leu Thr Asp Leu Pro Gln Asp Ile Asp
 100 105 110
 Arg Leu Glu Glu Leu Gln Ser Phe Leu Leu Tyr Lys Asn Lys Leu Thr
 115 120 125
 Tyr Leu Pro Tyr Ser Met Leu Asn Leu Lys Lys Leu Thr Leu Leu Val
 130 135 140
 Val Ser Gly Asp His Leu Val Glu Leu Pro Thr Ala Leu Cys Asp Ser
 145 150 155 160
 Ser Thr Pro Leu Lys Phe Val Ser Leu Met Asp Asn Pro Ile Asp Asn
 165 170 175
 Ala Gln Cys Glu Asp Gly Asn Glu Ile Met Glu Ser Glu Arg Asp Arg
 180 185 190
 Gln His Phe Asp Lys Glu Val Met Lys Ala Tyr Ile Glu Asp Leu Lys
 195 200 205
 Glu Arg Glu Ser Val Pro Ser Tyr Thr Thr Lys Val Ser Phe Ser Leu
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 Gln Leu
 225